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RAW SEQUENCE LISTING DATE: 03/21/2002 PATENT APPLICATION: US/10/071,751 TIME: 15:52:05

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Output Set: N:\CRF3\03212002\J071751.raw

SEQUENCE LISTING

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3 (1) GENERAL INFORMATION:
      5
             (i) APPLICANT: Hunter, Shirley Wu
      6
                            Sim, Gek-Kee
      7
                            Weber, Eric R.
      9
            (ii) TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS AND
                                      APPARATUS TO COLLECT SUCH PROTEINS
     10
     12
           (iii) NUMBER OF SEQUENCES: 88
     14
            (iv) CORRESPONDENCE ADDRESS:
     15
                  (A) ADDRESSEE: SHERIDAN ROSS P.C.
                  (B) STREET: 1560 BROADWAY, SUITE 1200
     16
     17
                  (C) CITY: DENVER
                                                             ENTERED
     18
                  (D) STATE: CO
     19
                  (E) COUNTRY: U.S.A.
     20
                  (F) ZIP: 80202
             (V) COMPUTER READABLE FORM:
     22
                  (A) MEDIUM TYPE: Floppy disk
     23
                  (B) COMPUTER: IBM PC compatible
     24
     25
                  (C) OPERATING SYSTEM: PC-DOS/MS-DOS
     26
                  (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
     28
            (vi) CURRENT APPLICATION DATA:
C--> 29
                  (A) APPLICATION NUMBER: US/10/071,751
C--> 30
                  (B) FILING DATE: 07-Feb-2002
     31
                  (C) CLASSIFICATION:
     33
           (vii) PRIOR APPLICATION DATA:
     34
                  (A) APPLICATION NUMBER: 09/171,156
     35
                  (B) FILING DATE: 1998-10-09
     39
          (viii) ATTORNEY/AGENT INFORMATION:
                  (A) NAME: Connell, Gary J.
     40
     41
                  (B) REGISTRATION NUMBER: 32,020
     42
                  (C) REFERENCE/DOCKET NUMBER: 2618-17-C4-PUS
            (ix) TELECOMMUNICATION INFORMATION:
     44
                  (A) TELEPHONE: 303/863-9700
     45
                  (B) TELEFAX: 303/863-0223
     46
     49 (2) INFORMATION FOR SEQ ID NO: 1:
             (i) SEQUENCE CHARACTERISTICS:
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                  (A) LENGTH: 26 amino acids
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                  (B) TYPE: amino acid
     54
                  (C) STRANDEDNESS:
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                  (D) TOPOLOGY: linear
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            (ii) MOLECULE TYPE: protein
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            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                       Met Arg Gly Asn His Val Phe Leu Glu Asp Gly Met Ala Asp Met Thr
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62
                       Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr
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     65
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                  (A) LENGTH: 12 amino acids
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                  (B) TYPE: amino acid
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                  (C) STRANDEDNESS:
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                  (D) TOPOLOGY: linear
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     75
            (ii) MOLECULE TYPE: protein
            (ix) FEATURE:
     77
                  (A) NAME/KEY: Xaa = Tyr or Asp
     78
     79
                  (B) LOCATION: 5
            (ix) FEATURE:
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                  (A) NAME/KEY: Xaa = any amino acid
     82
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                  (B) LOCATION: 6
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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                       Lys Tyr Arg Asn Xaa Xaa Thr Asn Asp Pro Gln Tyr
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                  (A) LENGTH: 27 amino acids
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                  (B) TYPE: amino acid
                  (C) STRANDEDNESS:
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            (ii) MOLECULE TYPE: protein
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     101
                         Glu Ile Lys Arg Asn Asp Arg Glu Pro Gly Asn Leu Ser Lys Ile Arg
     103
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                                                              10
                         Thr Val Met Asp Lys Val Ile Lys Gln Thr Gln
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     107
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                   (A) LENGTH: 23 amino acids
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                   (B) TYPE: amino acid
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                   (D) TOPOLOGY: linear
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             (ii) MOLECULE TYPE: protein
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             (ix) FEATURE:
     120
                   (A) NAME/KEY: Xaa = Ala or His
                    (B) LOCATION: 8
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                    (A) NAME/KEY: Xaa = Ala or His
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                    (B) LOCATION: 9
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             (xi) SEQUENCE DESCRIPTION: SEQ.ID NO: 4:
     127
                         Leu Lys Asp Asn Asp Ile Tyr Xaa Xaa Arg Asp Ile Asn Glu Ile Leu
W--> 129
                                                                                   15
     130
                                                               10
                         Arg Val Leu Asp Pro Ser Lys
     132
     133
                                     20
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Input Set : N:\Crf3\RULE60\10071751.txt
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135 (2) INFORMATION FOR SEQ ID NO: 5: (i) SEQUENCE CHARACTERISTICS: 137 (A) LENGTH: 27 amino acids 138 139 (B) TYPE: amino acid 140 (C) STRANDEDNESS: (D) TOPOLOGY: linear 141 (ii) MOLECULE TYPE: protein 143 (ix) FEATURE: 145 (A) NAME/KEY: Xaa = any amino acid 146 (B) LOCATION: 12 147 149 (ix) FEATURE: 150 (A) NAME/KEY: Xaa = any amino acid 151 (B) LOCATION: 18 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5: 153 Asn Tyr Gly Arg Val Gln Ile Glu Asp Tyr Thr Xaa Ser Asn His Lys W--> 155 156 10 W--> 158Asp Xaa Glu Glu Lys Asp Gln Ile Asn Gly Leu 159 161 (2) INFORMATION FOR SEQ ID NO: 6: (i) SEQUENCE CHARACTERISTICS: 163 164 (A) LENGTH: 18 amino acids 165 (B) TYPE: amino acid 166 (C) STRANDEDNESS: (D) TOPOLOGY: linear 167 (ii) MOLECULE TYPE: protein 169 171 (ix) FEATURE: (A) NAME/KEY: Xaa = any amino acid 172 173 (B) LOCATION: 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6: 176 W--> 178 Lys Tyr Arg Asn Xaa Tyr Thr Asn Asp Pro Gln Leu Lys Leu Leu Asp 179 181 Glu Gly 184 (2) INFORMATION FOR SEQ ID NO: 7: (i) SEQUENCE CHARACTERISTICS: 186 187 (A) LENGTH: 22 amino acids 188 (B) TYPE: amino acid 189 (C) STRANDEDNESS: 190 (D) TOPOLOGY: linear 192 (ii) MOLECULE TYPE: protein 194 (ix) FEATURE: (A) NAME/KEY: Xaa = any amino acid 195 196 (B) LOCATION: 13 198 (ix) FEATURE: 199 (A) NAME/KEY: Xaa = any amino acid 200 (B) LOCATION: 19 202 (ix) FEATURE: 203 (A) NAME/KEY: Xaa = any amino acid 204 (B) LOCATION: 21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

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RAW SEQUENCE LISTING

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DATE: 03/21/2002

209 1 5 10 15 W> 211 Tyr Pro Xaa Ala Xaa Leu 212 20 214 (2) INFORMATION FOR SEQ ID NO: 8: 216 (i) SEQUENCE CHARACTERISTICS: 217 (A) LENGTH: 20 base pairs 218 (B) TYPE: nucleic acid 219 (C) STRANDEDNESS: single 220 (D) TOPOLOGY: linear 222 (ii) MOLECULE TYPE: DNA (genomic) 224 (ix) FEATURE: 225 (A) NAME/KEY: misc_feature 226 (B) LOCATION: 120 227 (D) OTHER INFORMATION: /label= primer 229 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8: 231 TGRTTTCCWA TRAARTCTTC 233 (2) INFORMATION FOR SEQ ID NO: 9: 235 (i) SEQUENCE CHARACTERISTICS: 236 (A) LENGTH: 225 base pairs 237 (B) TYPE: nucleic acid 238 (C) STRANDEDNESS: single 239 (D) TOPOLOGY: linear 241 (ii) MOLECULE TYPE: DNA (genomic)	
212 214 (2) INFORMATION FOR SEQ ID NO: 8: 216	
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(B) LOCATION: 120 (D) OTHER INFORMATION: /label= primer (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8: TGRTTTCCWA TRAARTCTTC (33 (2) INFORMATION FOR SEQ ID NO: 9: (i) SEQUENCE CHARACTERISTICS: (a) LENGTH: 225 base pairs (b) TYPE: nucleic acid (c) STRANDEDNESS: single (d) TOPOLOGY: linear	
(D) OTHER INFORMATION: /label= primer (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8: TGRTTTCCWA TRAARTCTTC 133 (2) INFORMATION FOR SEQ ID NO: 9: 155 (i) SEQUENCE CHARACTERISTICS: 166 (A) LENGTH: 225 base pairs 177 (B) TYPE: nucleic acid 178 (C) STRANDEDNESS: single 179 (D) TOPOLOGY: linear	
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(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 225 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	20
(A) LENGTH: 225 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
237 (B) TYPE: nucleic acid 238 (C) STRANDEDNESS: single 239 (D) TOPOLOGY: linear	
(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
239 (D) TOPOLOGY: linear	
243 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:	
245 GAATTCGGCA CGAGTGAAAT TCAATATTTT GTTTTACATT AAATTTTTCA AATTCGATAT	60
	L20
249 AATGGTCACT GAAAAGTGTA AGTCAGGTGG AAATAATCCA AGTACAGAAG AGGTGTCAAT 1	180
251 ACCATCTGGG AAGCTTACTA TTGAAGATTT TTGTATTGGA AATCA 2	225
253 (2) INFORMATION FOR SEQ ID NO: 10:	
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256 (A) LENGTH: 15 base pairs	
257 (B) TYPE: nucleic acid	
258 (C) STRANDEDNESS: single	
259 (D) TOPOLOGY: linear	
261 (ii) MOLECULE TYPE: DNA (genomic)	
263 (ix) FEATURE:	
264 (A) NAME/KEY: misc_feature	
265 (B) LOCATION: 115	
266 (D) OTHER INFORMATION: /label= primer 268 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:	
268 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10: 270 AATTCGGCAC GAGTG	15
270 AATTCGGCAC GAGTG 272 (2) INFORMATION FOR SEQ ID NO: 11:	13
272 (2) INFORMATION FOR SEQ ID NOT IT: 274 (i) SEQUENCE CHARACTERISTICS:	
275 (A) LENGTH: 565 base pairs	
276 (B) TYPE: nucleic acid	
277 (C) STRANDEDNESS: single	
278 (D) TOPOLOGY: linear	
280 (ii) MOLECULE TYPE: cDNA	





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282	(ix) FEATURE:	
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284 287	(B) LOCATION: 45314 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:	
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290	Met Lys Phe Leu	50
291	1	
293	CTG GCA ATT TGC GTG TTG TGT GTT TTA TTA AAT CAA GTA TCT ATG TCA	104
294	Leu Ala Ile Cys Val Leu Cys Val Leu Asn Gln Val Ser Met Ser	
295	5 10 15 20	
297	AAA ATG GTC ACT GAA AAG TGT AAG TCA GGT GGA AAT AAT CCA AGT ACA	152
298	Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn Asn Pro Ser Thr	
299	25 30 35	
301	GAA GAG GTG TCA ATA CCA TCT GGG AAG CTT ACT ATT GAA GAT TTT TGT	200
302	Glu Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile Glu Asp Phe Cys	
303	40 45 50	
305	ATT GGA AAT CAT CAA AGT TGC AAA ATA TTT TAC AAA AGT CAA TGT GGA	248
306	Ile Gly Asn His Gln Ser Cys Lys Ile Phe Tyr Lys Ser Gln Cys Gly	
307	. 55 60 65	
309	TTT GGA GGT GGT TGT GGA AAC GGT GGT TCA ACA CGA CCA AAT CAA	296
310	Phe Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr Arg Pro Asn Gln	
311	70 75 80	244
313	AAA CAC TGT TAT TGC GAA TAACCATATT CCGGATGAAA GACCAAATTG	344
314	Lys His Cys Tyr Cys Glu	
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315	85 90	404
317	ATATAAATTA CTAAAATTAT GCTAGATAGC AATCATAAAA TTTTGAAGTT TTCAATGATC	404
317 319	ATATAAATTA CTAAAATTAT GCTAGATAGC AATCATAAAA TTTTGAAGTT TTCAATGATC CTAACATGTT TTGCCTCCAA TTTATTTTAA CAGCAAATTG CTGGAACTTA CCGTACCGTA	464
317 319 321	ATATAAATTA CTAAAATTAT GCTAGATAGC AATCATAAAA TTTTGAAGTT TTCAATGATC CTAACATGTT TTGCCTCCAA TTTATTTTAA CAGCAAATTG CTGGAACTTA CCGTACCGTA	464 524
317 319 321 323	ATATAAATTA CTAAAATTAT GCTAGATAGC AATCATAAAA TTTTGAAGTT TTCAATGATC CTAACATGTT TTGCCTCCAA TTTATTTTAA CAGCAAATTG CTGGAACTTA CCGTACCGTA	464
317 319 321 323 325 (2)	ATATAAATTA CTAAAATTAT GCTAGATAGC AATCATAAAA TTTTGAAGTT TTCAATGATC CTAACATGTT TTGCCTCCAA TTTATTTTAA CAGCAAATTG CTGGAACTTA CCGTACCGTA	464 524
317 319 321 323 325 (2) 327	ATATAAATTA CTAAAATTAT GCTAGATAGC AATCATAAAA TTTTGAAGTT TTCAATGATC CTAACATGTT TTGCCTCCAA TTTATTTTAA CAGCAAATTG CTGGAACTTA CCGTACCGTA	464 524
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317 319 321 323 325 (2) 327 328 329 330	ATATAAATTA CTAAAATTAT GCTAGATAGC AATCATAAAA TTTTGAAGTT TTCAATGATC CTAACATGTT TTGCCTCCAA TTTATTTTAA CAGCAAATTG CTGGAACTTA CCGTACCGTA	464 524
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317 319 321 323 325 (2) 327 328 329 330 332 334 336 337	ATATAAATTA CTAAAATTAT GCTAGATAGC AATCATAAAA TTTTGAAGTT TTCAATGATC CTAACATGTT TTGCCTCCAA TTTATTTTAA CAGCAAATTG CTGGAACTTA CCGTACCGTA	464 524
317 319 321 323 325 (2) 327 328 329 330 332 334 336 337 339	ATATAAATTA CTAAAATTAT GCTAGATAGC AATCATAAAA TTTTGAAGTT TTCAATGATC CTAACATGTT TTGCCTCCAA TTTATTTTAA CAGCAAATTG CTGGAACTTA CCGTACCGTA	464 524
317 319 321 323 325 (2) 327 328 329 330 332 334 336 337 339 340	ATATAAATTA CTAAAATTAT GCTAGATAGC AATCATAAAA TTTTGAAGTT TTCAATGATC CTAACATGTT TTGCCTCCAA TTTATTTTAA CAGCAAATTG CTGGAACTTA CCGTACCGTA	464 524
317 319 321 323 325 (2) 327 328 329 330 332 334 336 337 339 340 342	ATATAAATTA CTAAAATTAT GCTAGATAGC AATCATAAAA TTTTGAAGTT TTCAATGATC CTAACATGTT TTGCCTCCAA TTTATTTTAA CAGCAAATTG CTGGAACTTA CCGTACCGTA	464 524
317 319 321 323 325 (2) 327 328 329 330 332 334 336 337 339 340 342 343	ATATAAATTA CTAAAATTAT GCTAGATAGC AATCATAAAA TTTTGAAGTT TTCAATGATC CTAACATGTT TTGCCTCCAA TTTATTTTAA CAGCAAATTG CTGGAACTTA CCGTACCGTA	464 524
317 319 321 323 325 (2) 327 328 329 330 332 334 336 337 339 340 342 343 345	ATATAAATTA CTAAAATTAT GCTAGATAGC AATCATAAAA TTTTGAAGTT TTCAATGATC CTAACATGTT TTGCCTCCAA TTTATTTTAA CAGCAAATTG CTGGAACTTA CCGTACCGTA	464 524
317 319 321 323 325 (2) 327 328 329 330 332 334 336 337 339 340 342 343 345 346	ATATAAATTA CTAAAATTAT GCTAGATAGC AATCATAAAA TTTTGAAGTT TTCAATGATC CTAACATGTT TTGCCTCCAA TTTATTTTAA CAGCAAATTG CTGGAACTTA CCGTACCGTA	464 524
317 319 321 323 325 (2) 327 328 329 330 332 334 336 337 339 340 342 343 345 346 348	ATATAAATTA CTAAAATTAT GCTAGATAGC AATCATAAAA TTTTGAAGTT TTCAATGATC CTAACATGTT TTGCCTCCAA TTTATTTTAA CAGCAAATTG CTGGAACTTA CCGTACCGTA	464 524
317 319 321 323 325 (2) 327 328 329 330 332 334 336 337 339 340 342 343 345 345 346 348	ATATAAATTA CTAAAATTAT GCTAGATAGC AATCATAAAA TTTTGAAGTT TTCAATGATC CTAACATGTT TTGCCTCCAA TTTATTTTAA CAGCAAATTG CTGGAACTTA CCGTACCGTA	464 524
317 319 321 323 325 (2) 327 328 329 330 332 334 336 337 339 340 342 343 345 345 346 348 349 351	ATATAAATTA CTAAAATTAT GCTAGATAGC AATCATAAAA TTTTGAAGTT TTCAATGATC CTAACATGTT TTGCCTCCAA TTTATTTTAA CAGCAAATTG CTGGAACTTA CCGTACCGTA	464 524
317 319 321 323 325 (2) 327 328 329 330 332 334 336 337 339 340 342 343 345 346 348 349 351 352	ATATAAATTA CTAAAATTAT GCTAGATAGC AATCATAAAA TTTTGAAGTT TTCAATGATC CTAACATGTT TTGCCTCCAA TTTATTTTAA CAGCAAATTG CTGGAACTTA CCGTACCGTA	464 524





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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the $\langle 220 \rangle$ to $\langle 223 \rangle$ fields of each sequence which presents at least one n or Xaa.

Seq#:2; Xaa Pos.5,6
Seq#:4; Xaa Pos.8,9
Seq#:5; Xaa Pos.12,18
Seq#:6; Xaa Pos.5
Seq#:7; Xaa Pos.13,19,21
Seq#:29; Xaa Pos.379
Seq#:30; Xaa Pos.379
Seq#:35; N Pos. 192
Seq#:70; Xaa Pos.1,24

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The rules require that a line not exceed 72 characters in length. This includes spaces.

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Seq#:10; Line(s) 270
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Seq#:13; Line(s) 370,374,378,382,386,390
Seq#:15; Line(s) 440
Seq#:16; Line(s) 459
Seq#:17; Line(s) 477,479,483,487,491,495,500,504,508,512,516,520,524,526
Seq#:17; Line(s) 528,530,532
Seq#:19; Line(s) 587,589,591,593,595,597,599,601
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Seq#:20; Line(s) 731,735,739,743,747,751,755,759,763,767,771,775,779,783
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Seq#:20; Line(s) 843
Seq#:22; Line(s) 1045,1049,1053,1057,1061,1065,1070,1074,1078
Seq#:24; Line(s) 1136,1140,1144,1148,1152,1156
Seq#:26; Line(s) 1205,1209,1213,1217,1221,1225,1229,1233,1237,1241,1245
Seq#:26; Line(s) 1249,1254,1258,1262,1266,1270,1274,1278,1282,1286,1290
Seq#:26; Line(s) 1294,1298,1302,1306,1310,1314,1318,1322,1326,1328,1330
Seq#:26; Line(s) 1332,1334
Seq#:28; Line(s) 1446,1448,1450,1452,1454,1456,1458,1460,1462,1464,1466
Seq#:28; Line(s) 1468,1470,1472,1474,1476,1478,1480,1482,1484,1486,1488
Seq#:28; Line(s) 1490,1492
Seq#:29; Line(s) 1514,1518,1522,1526,1530,1534,1538,1542,1546,1550,1554
Seq#:29; Line(s) 1558,1562,1566,1570,1574,1578,1582,1586,1590,1594,1598
Seq#:29; Line(s) 1602,1606,1610,1614,1618,1622,1626,1630,1634,1638,1642
Seq#:29; Line(s) 1646,1650,1654,1658
Seq#:31; Line(s) 1801,1803,1805,1807,1809
Seq#:32; Line(s) 1823,1825,1827,1829,1831,1833
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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 03/21/2002 PATENT APPLICATION: US/10/071,751 TIME: 15:52:06

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Seg#:33; Line(s) 1847,1849,1851,1853,1855,1857,1859
Seq#:34; Line(s) 1873,1875,1877,1879,1881
Seq#:35; Line(s) 1895,1897,1899,1901
Seq#:36; Line(s) 1919,1923,1927,1931,1935,1939,1943,1947
Seq#:38; Line(s) 2001,2005,2009,2013,2017,2021,2025,2029,2033,2037
Seq#:40; Line(s) 2089,2091,2093,2095,2097,2099
Seq#:41; Line(s) 2113,2115,2117,2119,2121,2123,2125,2127,2129
Seq#:42; Line(s) 2143,2145,2147,2149,2151,2153,2155,2157,2159,2161,2163
Seq#:43; Line(s) 2177,2179,2181,2183,2185,2187,2189,2191
Seq#:44; Line(s) 2205,2207,2209,2211,2213
Seq#:45; Line(s) 2227,2229,2231,2233,2235,2237,2239
Seq#:46; Line(s) 2253,2255,2257,2259,2261
Seq#:47; Line(s) 2275,2277,2279,2281,2283,2285,2287,2289,2291,2293,2295
Seq#:48; Line(s) 2313,2317,2321,2325,2329,2333,2337,2341,2345,2349,2353
Seq#:48; Line(s) 2357
Seq#:50; Line(s) 2424,2428,2432,2436,2440,2444,2448,2452,2456
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Seq#:52; Line(s) 2550
Seq#:54; Line(s) 2593,2595,2597,2599,2601,2603,2605,2607,2609,2611
Seq#:55; Line(s) 2629,2633,2637,2641,2645,2649
Seq#:57; Line(s) 2694,2696,2698,2700,2702
Seq#:58; Line(s) 2720,2724,2728,2732,2736
Seq#:60; Line(s) 2779,2781,2783,2785
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Seq#:61; Line(s) 2845,2847,2849,2851,2853,2855,2857,2859
Seq#:63; Line(s) 2914,2916,2918,2920,2922,2924,2926,2928,2930,2932,2934
Seq#:63; Line(s) 2936,2938,2940,2942,2944,2946
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Seq#:64; Line(s) 3052,3056,3058
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Seq#:66; Line(s) 3174,3176,3178,3180,3182,3184,3186,3188,3190,3192
Seq#:67; Line(s) 3211,3215,3219,3223,3227,3231,3235,3239,3243,3247,3251
Seq#:67; Line(s) 3255,3259,3263,3267,3271,3275,3279,3283,3287,3291,3295
Seq#:67; Line(s) 3299
Seq#:69; Line(s) 3395,3397,3399,3401,3403,3405,3407,3409,3411,3413,3415
Seq#:69; Line(s) 3417,3419,3421,3423,3425,3427,3429
Seq#:71; Line(s) 3475,3479,3483,3487,3491,3495,3499,3503,3507
Seq#:73; Line(s) 3562,3564,3566,3568,3570,3572,3574
Seq#:74; Line(s) 3593,3597,3601,3605,3609,3613,3615,3617
Seq#:76; Line(s) 3657,3659,3661,3663,3665,3667,3669
Seq#:79; Line(s) 3733
Seq#:80; Line(s) 3752
Seq#:81; Line(s) 3771
Seq#:82; Line(s) 3790
Seq#:83; Line(s) 3809
Seq#:84; Line(s) 3828.
Seq#:85; Line(s) 3847
Seq#:86; Line(s) 3866
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RAW SEQUENCE LISTING ERROR SUMMARY PATENT APPLICATION: US/10/071,751

DATE: 03/21/2002 TIME: 15:52:06

Input Set : N:\Crf3\RULE60\10071751.txt
Output Set: N:\CRF3\03212002\J071751.raw

Seq#:88; Line(s) 3907





DATE: 03/21/2002

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/071,751

TIME: 15:52:06

Input Set : N:\Crf3\RULE60\10071751.txt Output Set: N:\CRF3\03212002\J071751.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:] L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:] L:88 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0 L:129 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0 L:155 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0 L:158 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:16 L:178 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0 $L:208\ M:341\ W:$ (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0 L:211 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:16 L:1607 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:1152 L:1747 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:368 L:3452 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70 after pos.:0 L:3455 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70 after pos.:16